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BECKER, DOUGLAS KEITH
HAFNER, GREGORY JOHN
YANG, ILIN

<120> TRANSCRIPTIONAL CONTROL ELEMENT, CHIMERIC CONSTRUCTS
AND USES THEREFOR

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<170> PatentIn Ver. 3.3

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<210> 3

<211> 146

<212> PRT

<213> Taro bacilliform virus

<400> 3

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  1                      5                      10                      15

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Arg Arg Ala Asp Leu Ser Tyr Leu Asp Leu Ala Thr Thr Thr Lys Pro
      20                      25                      30

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Ser Ala Ser Gln Leu Ala His Asn Leu Gln Val Ile Phe Asp Arg Leu
    35                      40                      45

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Ser Leu His Ser Ser Val Ser Ile Lys Glu His Tyr Glu Val Val Ser
50 55 60

Lys Leu His Ser Leu Glu Lys Ser Ile Glu Glu Leu Lys Ser Glu Leu
65 70 75 80

Thr Thr Val Lys Arg Ala Leu Thr Ser Ile Gln Lys Glu Val Phe Thr
85 90 95

His Lys Pro Leu Thr Ala Gln Glu Val Gln Thr Leu Ala Gln Ser Leu
100 105 110

Ile Lys Glu Pro Lys Gln Ile Glu Gln Gln Ala Val Phe Leu Leu Lys
115 120 125

Glu Leu Lys Glu Gln Thr Ala Lys Ile Gln Ala Leu Leu His Glu Leu
130 135 140

Lys Ser
145

<210> 4

<211> 144

<212> PRT

<213> Taro bacilliform virus

<400> 4

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Glu Thr Lys Val Leu Gly Asp Pro Ser Val Gly Phe Ser Glu Ile Pro
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Thr Thr Ala Ile Gly Thr Ala Thr Gly Phe Ser Thr Leu Tyr Lys Gln
35 40 45

Asn Asn Thr Ile Ile Asn Leu Leu Ile Ser Leu His Lys Lys Val Asp
50 55 60

Ser Leu Ser Lys Lys Thr Asp Val Asp Glu Leu Ala Thr Glu Leu Ser
65 70 75 80

Lys Leu Thr Ile Lys Asp Thr Pro Lys Val Lys Ala Lys Thr Pro Leu
85 90 95

Tyr Val Phe Lys Ser Pro Arg Leu Ile Leu Glu Glu Glu Arg Tyr Lys
100 105 110

Ile Gly Leu Pro Pro Thr Thr Thr Asp Trp Thr Trp Pro Val Gly His
115 120 125

Pro Phe Ala Pro Pro Pro Lys Thr Ser Thr Lys Ala Ser Thr Ser Ser
130 135 140

<210> 5
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 <212> PRT
 <213> Taro bacilliform virus

<400> 5
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 Arg Val Arg His Thr Ala Glu Arg Ala Ala Arg Arg Ile Phe Pro Gly
 35 40 45
 Arg Phe Asn Arg Thr Leu Glu Ser Gln Ile Asn Pro Glu Ala Glu Ile
 50 55 60
 Arg Leu Ser Gln Gln Arg Arg Ala Ala Met Val Pro Ala Glu Val Leu
 65 70 75 80
 Tyr Asn Thr Ser Pro Ser Thr Arg Asn Gln Lys Val Tyr Gln His Tyr
 85 90 95
 Ser Glu Glu Arg Ile Leu Cys Thr Gly Gln Asn Gln Gln Leu Asn Leu
 100 105 110
 Pro Phe Ile Asn Glu Ser Ser Tyr Arg Ala Leu Arg Glu Ser Gly Gln
 115 120 125
 Gln His Leu His Ile Gly Leu Ile Met Ile Arg Val His Pro Leu His
 130 135 140
 Arg Arg Asn Ala Gly Thr Thr Ala Leu Ile Val Pro Arg Asp Ile Arg
 145 150 155 160
 Trp Asn Asp Asp Arg Ser Ile Ile Gly Thr Met Glu Ile Asp Leu Ser
 165 170 175
 Ala Gly Ser Gln Ile Val Tyr Ile Ala Pro Asn Ile Met Leu Ser Val
 180 185 190
 Glu Asp Phe Tyr Arg Asn Ile Gln Leu Ala Ile Gln Thr Gln Gly Tyr
 195 200 205
 Glu Asn Trp Asn Ser Ala Glu Ser Asn Leu Leu Ile Ser Arg Ala Leu
 210 215 220
 Ile Gly Arg Leu Thr Asn Asp Ser Phe Thr Gly Phe Gln Tyr Asn Ile
 225 230 235 240
 Ser Asn Val Ala Glu Tyr Leu His Ser His Gly Val Gln Ala Ile Glu
 245 250 255
 Gly Gln Ala His Pro Arg Thr Leu Gly Asn Arg Trp Ile Leu Gln Ala
 260 265 270

Pro Ala Pro Pro Arg Ser Leu Val Pro Gln Asn Val Glu Thr Thr Thr
 275 280 285
 Leu Leu Asp Gly Asn Val Ser Ile Arg Phe Ser Asn Tyr His Gln Ala
 290 295 300
 Pro Val Asn Asp Thr Gln Asp Asn Ser His Pro Asp Ile Gln Glu Asp
 305 310 315 320
 Glu Asn Gln Phe Ile Gly Phe Leu Ser Asp Leu Gly Glu Glu Tyr Glu
 325 330 335
 Leu Glu Tyr Pro Ser Phe Thr Pro Val His Ala Asp Glu Phe Ile Phe
 340 345 350
 Ile Ile Ile Asn Gly Glu Glu Ile Pro Asp Asp Phe Val Ser Ser Phe
 355 360 365
 Cys Ser Asn Phe Ser Pro Pro Pro Ile Pro Glu Pro Glu Pro Thr Ala
 370 375 380
 Ile Glu Glu Thr Ala Phe Thr Leu Glu Glu Gln Phe Asn Asp Leu Asp
 385 390 395 400
 Tyr Pro Thr Leu Ile Ser Met Glu Lys Gln Leu Val Gln Ser Ser Val
 405 410 415
 Thr Ser Ala Tyr Asn Pro Pro Thr Glu Pro Leu Met Gly Gln Val Val
 420 425 430
 Tyr Pro Pro Ala Ser Ala Pro Arg Pro Gln Ala Glu Thr Ser Ser Thr
 435 440 445
 Ser Glu Arg Phe Lys Asn Phe Arg Ala Lys Pro Tyr Ser Thr Pro Thr
 450 455 460
 Ile Phe Leu Pro Pro Ala Tyr Asn Gln Gln Gly Ala Ile Leu Val Leu
 465 470 475 480
 Pro Asp Asp Ile Gly Leu Tyr Glu Asp Thr Ile Ser Arg Trp Glu Ser
 485 490 495
 Ile Thr Leu Asn Met Met Asn Glu Lys Val Trp Pro Ser Asn Glu Ala
 500 505 510
 Lys Ala Lys Tyr Met Glu Asn Leu Leu Gly Glu Met Glu Lys Lys Thr
 515 520 525
 Trp Ile Gln Trp Arg Thr Thr Tyr Val Ser Glu Tyr Asp Ala Leu Val
 530 535 540
 Gln Gln Ser Asp Glu Thr Gln Asn Leu Leu Ser Gln Val Arg Arg Ile
 545 550 555 560
 Phe Leu Leu Gln Asp Pro Tyr Gln Gly Ser Thr Ala Glu Gln Asp Gln
 565 570 575

Ala	Tyr	Asn	Asp	Leu	Glu	Arg	Ile	Ser	Cys	Asp	Asn	Ile	Lys	Asp	Leu	580	585	590	
Ile	Pro	Tyr	Leu	Ile	Gln	Phe	Arg	Asn	Leu	Ala	Ala	Lys	Ser	Gly	Arg	595	600	605	
Leu	Phe	Leu	Gly	Pro	Glu	Leu	Ser	Glu	Lys	Leu	Phe	Arg	Lys	Met	Pro	610	615	620	
Pro	Leu	Ile	Gly	Lys	Glu	Ile	Glu	Thr	Ala	Phe	Ile	Ala	Lys	His	Gly	625	630	635	640
Asn	Ala	Asn	Ile	Thr	Val	Met	Pro	Arg	Ile	His	Phe	Ala	Tyr	His	Tyr	645	650	655	
Leu	Ala	Glu	Leu	Cys	Lys	Lys	Ala	Ala	Leu	Gln	Arg	Ser	Leu	Lys	Asp	660	665	670	
Leu	Ser	Phe	Cys	Asn	Gln	Ile	Pro	Leu	Pro	Gly	Ile	Tyr	Thr	Lys	Gly	675	680	685	
Asn	Lys	Lys	Phe	Gly	Leu	Arg	Lys	Ala	Arg	Thr	Tyr	Lys	Gly	Lys	Pro	690	695	700	
His	Pro	Thr	His	Val	Arg	Val	Phe	Lys	Lys	Ala	Lys	Tyr	Gln	Arg	Thr	705	710	715	720
Lys	Lys	Cys	Lys	Cys	Phe	Ile	Cys	Gly	Glu	Pro	Gly	His	Phe	Ala	Arg	725	730	735	
Glu	Cys	Thr	Lys	Gln	Arg	Gly	Asn	Ile	Val	Arg	Ala	Thr	Val	His	Gln	740	745	750	
Glu	Leu	Ala	Ile	Pro	Asp	Asn	Phe	Asp	Val	Val	Ser	Val	Asp	Ala	Asp	755	760	765	
Glu	Ser	Asp	Ser	Ser	Gly	Ile	Tyr	Ser	Tyr	Ser	Glu	Asn	Glu	Ala	Pro	770	775	780	
Leu	Gln	Glu	Val	Asn	Ser	Phe	Ile	His	Asp	Glu	Asn	Ile	Phe	Phe	Leu	785	790	795	800
Ser	Asp	Ala	Asp	Glu	Phe	Glu	Ser	Pro	Gln	Gln	His	Leu	His	Glu	Thr	805	810	815	
Val	Asn	Met	Leu	Gln	Ser	Arg	Ser	Ala	Tyr	Leu	Pro	Gln	Val	Ala	Val	820	825	830	
Gly	Glu	Glu	Lys	Leu	Asn	Cys	Ser	His	Ile	Trp	Leu	Gln	Asp	Val	Asp	835	840	845	
Ile	Pro	Ser	Asp	Lys	His	Lys	Cys	His	Thr	Cys	Arg	Arg	Asp	Thr	Gln	850	855	860	
Lys	His	Tyr	Arg	Leu	Glu	Cys	Gln	Lys	Cys	Lys	Phe	Leu	Val	Cys	Ser	865	870	875	880

Leu Cys Thr Ile Pro Tyr Leu Gly Ile Thr Met Gln Phe Arg Gln Lys
 885 890 895
 Gln Lys Ser Gln Pro Glu Asn Pro Asn Leu Val Arg Glu Leu Leu Glu
 900 905 910
 His Ala Ile Phe Leu Glu Glu Lys Cys Lys Asn Gln Glu Leu Leu Ser
 915 920 925
 Glu Thr Gln Ile Glu Arg Ile Val Ser Ser Glu Lys Gln Val Lys Phe
 930 935 940
 Tyr Gly Ile Leu Pro Thr Lys Lys Ser Asn Lys Ser Ala Gly Tyr Asp
 945 950 955 960
 Leu Gln Ser Asn Ile Asp Ile Glu Ile Pro Pro Gly Lys Cys Thr Val
 965 970 975
 Ile Ser Thr Gly Thr Phe Leu Gln Met Pro Asp Asn Met Tyr Gly Arg
 980 985 990
 Leu Val Glu Arg Thr Ser Leu Ala Ile Gln Gly Ile Thr Val Gln Gly
 995 1000 1005
 Gly Val Ile Asp Pro Asp Phe Thr Gly Glu Ile Gln Ile Val Leu Phe
 1010 1015 1020
 Asn His Asn Thr Ala Pro Tyr Pro Val Lys Lys Thr Tyr Arg Leu Ala
 1025 1030 1035 1040
 Gln Ile Ile Phe Glu Lys Phe Tyr Thr Pro Ile Phe Ile Gln Glu Pro
 1045 1050 1055
 Phe Thr Ser Thr Gln Gln Gly Ser Ser Asn Phe Gly Ser Thr Ala Lys
 1060 1065 1070
 Pro Leu Gln Ile Thr Glu Asn Ile Glu Val Met Ser Glu Thr Val Ala
 1075 1080 1085
 Asn Gln Val Ala Lys Ser Ser Val Leu Pro Arg Leu Tyr Ser Ile Gln
 1090 1095 1100
 Ala His Ile His Ile Ala Pro Asp Ile Val Ile Ser Thr Thr Ala Ile
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 1125 1130 1135
 Glu Ala Ala Lys Glu Gln Leu Asn Tyr Lys Val Asn Ile Ser Gly Ile
 1140 1145 1150
 Ser Ser Gln Gln Gln Ile Gln His Arg Leu Lys Arg Gly Thr Leu Glu
 1155 1160 1165
 Ile Ala Ser Asn Lys Tyr Ala Leu Pro Leu Cys Tyr Ile Ile Glu Leu
 1170 1175 1180

Asn Asp Lys Asp Asp Phe Ser Met Ile Leu Gly Cys Asn Phe Phe Lys
 1185 1190 1195 1200
 His Met Gly Gly Gly Met Arg Phe Glu Gly Pro His Val Thr Phe Tyr
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 Lys Gly Ile Thr Thr Leu Ser Thr Ser Tyr Ala Asn Thr Gly Ile Asp
 1220 1225 1230
 Thr Glu His Glu Gln Ile Thr Ser Thr Thr Ser Gln Ser Phe Lys Glu
 1235 1240 1245
 Arg Phe Ser Pro Leu Met Asn Glu Leu Lys Ala Ala Gly Tyr Ile Gly
 1250 1255 1260
 Glu Asp Pro Leu Lys His Trp Ser Lys Asn Lys Val Thr Cys Lys Leu
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 Asp Leu Lys Asn Thr Glu Ile Thr Ile Gln Asp Lys Pro Leu Arg His
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 Ile Lys Gly Lys Glu Arg Met Val Phe Asn Tyr Lys Ala Leu Asn Asp
 1345 1350 1355 1360
 Asn Thr Tyr Lys Asp Gln Tyr Ser Leu Pro Asn Ile Gln Leu Ile Leu
 1365 1370 1375
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 Gly Phe His Gln Val Ala Met Asp Pro Asp Ser Val Glu Trp Thr Ala
 1395 1400 1405
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 1410 1415 1420
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 1425 1430 1435 1440
 Lys Gly Cys Glu Lys Phe Leu Ala Val Tyr Ile Asp Asp Ile Leu Val
 1445 1450 1455
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 1475 1480 1485

Ile Ala Val Arg Glu Val Asn Phe Leu Gly Ala Thr Ile Gly Ser Arg
 1490 1495 1500
 Lys Val Lys Leu Gln Glu Asn Ile Ile Lys Lys Ile Leu Asp Phe Asp
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 1525 1530 1535
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 1540 1545 1550
 Pro Leu Tyr Ser Lys Thr Ser Ile Tyr Gly Asp Ile Arg Phe Ser Ala
 1555 1560 1565
 Ser Asp Trp Lys Leu Ile Asn Glu Ile Lys Ala Ile Val Glu Lys Leu
 1570 1575 1580
 Pro Pro Leu Asp Tyr Pro Pro Glu Gln Ala Tyr Ile Ile Ile Glu Ser
 1585 1590 1595 1600
 Asp Gly Cys Met Glu Gly Trp Gly Ala Ile Cys Lys Trp Lys Leu Ala
 1605 1610 1615
 Glu Tyr Asp Pro Lys Ser Ser Glu Gln Ile Cys Ala Tyr Ala Ser Gly
 1620 1625 1630
 Lys Phe Ser Pro Ile Lys Ser Thr Ile Asp Ala Glu Ile Thr Ala Ala
 1635 1640 1645
 Met Glu Gly Leu Glu Ala Phe Lys Ile His Tyr Leu Asp Lys Gln Lys
 1650 1655 1660
 Ile Thr Leu Arg Thr Asp Cys Gln Ala Ile Ile Ser Phe Cys Asn Lys
 1665 1670 1675 1680
 Thr Ser Val Asn Lys Pro Ser Arg Val Arg Trp Leu Lys Phe Ile Asp
 1685 1690 1695
 Tyr Ile Thr Asn Thr Gly Ile Asp Val Lys Phe Glu His Ile Asp Ala
 1700 1705 1710
 Lys Asn Asn Val Leu Ala Asp Thr Leu Ser Arg Leu Val Asn Thr Leu
 1715 1720 1725
 Gln Asp Leu Pro Trp Leu Asp Glu Pro His Gln Asp Gln Thr Val Ser
 1730 1735 1740
 Leu Met Gln Glu Ile Glu Asp Ala Pro Leu Glu Ile Lys Gln Arg Ser
 1745 1750 1755 1760
 Leu Thr Cys Leu Gln Arg Leu Ile Cys Arg Ser Phe Met Glu Asp Ser
 1765 1770 1775
 Thr Glu Glu Ala Ile His Phe Leu Glu Asp Asp Lys Ile Glu Pro Thr
 1780 1785 1790

Ala Glu Ser Ser Thr Pro Ile Thr Leu Asp Glu Phe Ser Arg Lys Arg
 1795 1800 1805

Phe Gln Glu His Thr Asp Leu Leu Glu Glu Phe Gln Leu Thr Leu Leu
 1810 1815 1820

Gln Ile Asn Leu Leu Glu Ala Ser Leu His Glu Arg Leu Met Lys Cys
 1825 1830 1835 1840

Gln Ser Tyr Ala Thr Arg Asp Asn Phe Trp Gly Asp Trp Leu Pro Glu
 1845 1850 1855

Ala Arg Arg Asp Leu Leu Gln Ile Gln Leu Ala Lys Glu Ile Ile Glu
 1860 1865 1870

Lys Val Arg Glu Lys Leu His Ser Ile
 1875 1880

<210> 6

<211> 1190

<212> DNA

<213> Taro bacilliform virus

<400> 6

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taacactttg caggatttgc catgggctaga tgaacctcat caggatcaaa cagtctccct 180
gatgcaggaa attgaagatg cacctcttga aatcaagcag cgttctttaa cctgcttaca 240
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<210> 7

<211> 598

<212> DNA

<213> Taro bacilliform virus

<400> 7

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aaaagcagat gccatcaact ttattcgagt tgagcctcgg ggagccgctc gtttaaagat 240
gctcttttga aaatgacagc gcgtgggtgc atgtcattct cactttttct ttaatgcgtc 300
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ccctcagaag aacggcaagc cggaaacacc gaacttccca ttcttctctt gagtctttcc 480
tttgagcttg agcttgtgtg taatctttca tagtttctaa gtctccgaag aacgagcacc 540
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<210> 8

<211> 529

<212> DNA

<213> Taro bacilliform virus

<400> 8

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tgccatcaac tttattcgag ttgagcctcg gggagccgct cgtttaaaga tgctcttttg 180
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gaacggcaag ccgaaacac cgaacttccc attcttctct tgagtctttc ctttgagctt 420
gagcttgtgt gtaatctttc atagtttcta agtctccgaa gaacgagcac cgtctcgtga 480
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<210> 9

<211> 261

<212> DNA

<213> Taro bacilliform virus

<400> 9

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ccattcttct cttgagctct tcctttgagc ttgagcttgt gtgtaatctt tcatagtttc 180
taagtctccg aagaacgagc accgtctcgt gaaggagccg atccttttcc aaccacactt 240
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261

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<210> 10

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<220>

<221> modified_base

<222> (6)

<223> inosine

<220>

<221> modified_base

<222> (12)

<223> inosine

<220>
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 <223> inosine

 <400> 10
 atgccnttyg gnaaraaygc ncc

23

<210> 11
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
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<220>
 <221> modified_base
 <222> (10)
 <223> inosine

<220>
 <221> modified_base
 <222> (13)
 <223> inosine

<220>
 <221> modified_base
 <222> (16)
 <223> inosine

<220>
 <221> modified_base
 <222> (22)
 <223> inosine

<400> 11
 ccayttrcan acnscncccc ancc

24

<210> 12
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 12
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23

<210> 13
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 13
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<210> 14
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 14
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<210> 15
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 15
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<210> 16
 <211> 12
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 16
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<210> 17
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 17

ctgcagatag gattccttgt gtgtg

25

<210> 18

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 18

ccatgggctc tgataccaag gtag

24

<210> 19

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 19

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20

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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic primer

<400> 20

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23

<210> 21

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28

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12